

RAW SEQUENCE LISTING

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Application Serial Number: 10/561, 015
Source: IFWP
Date Processed by STIC: 12/30/2005

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IFWP

RAW SEQUENCE LISTING

DATE: 12/30/2005

PATENT APPLICATION: US/10/561,015

TIME: 09:36:55

Input Set : A:\Sequence Listing PCTUS04019934.txt

Output Set: N:\CRF4\12302005\J561015.raw

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3 <110> APPLICANT: Felsenfeld, Dan P.
4     Verse-Pierluissi, Maria A.
6 <120> TITLE OF INVENTION: METHODS AND AGENTS FOR TREATING AXONAL DAMAGE, INHIBITION OF
7     NEUROTRANSMITTER RELEASE AND PAIN TRANSMISSION, AND BLOCKING
8     CALCIUM INFLUX IN NEURONS
10 <130> FILE REFERENCE: 02420/100M761-US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/561,015
C--> 12 <141> CURRENT FILING DATE: 2005-12-16
12 <150> PRIOR APPLICATION NUMBER: 60/480,092
13 <151> PRIOR FILING DATE: 2003-06-19
15 <150> PRIOR APPLICATION NUMBER: PCT/US04/19934
16 <151> PRIOR FILING DATE: 2004-06-21
18 <160> NUMBER OF SEQ ID NOS: 27
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 12
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: synthetic protein
30 <400> SEQUENCE: 1
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38 <212> TYPE: PRT
39 <213> ORGANISM: artificial sequence
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51 <211> LENGTH: 28
52 <212> TYPE: PRT
53 <213> ORGANISM: artificial sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: synthetic protein
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61 1           5           10           15
64 Gln Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Phe
65           20           25

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68 <210> SEQ ID NO: 4
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70 <212> TYPE: DNA
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76 gctcatacag attcctgatg aatataaagg acaccatgta ctagagccac ctgtcatcac 120
78 ggaacagtct ccacggcgcc tggttgtctt cccaacagat gacataagcc tcaaagtga 180
80 agccagaggc agaccccaag tggagttccg ctggacgaaa gatggcatcc acttcaaacc 240
82 taaggaagaa ttgggtgtag tggtagacga ggcaccctat tctggctcct tcaccatcga 300
84 aggcaacaac agctttgccc agaggtttca gggcatctat cgctgctatg ccagcaataa 360
86 tctaggaact gccatgtcgc atgagatcca gctcgtggct gagggtgccc ccaaaggcc 420
88 gaaggagact gtaaaacccg tggaagtgga ggaaggagaa tcagtagttc taccttgcaa 480
90 tcctccaccc agtgcagccc cacttaggat ctactggatg aacagcaaga ttttgacat 540
92 caaacaagat gagcgggtgt ccatgggcca gaatggagac ctatattttg ccaatgtgct 600
94 tactcagac aatcattcag actacatctg caatgccac ttccctggca cccggaccat 660
96 cattcaaaag gaacctattg acctccgggt caagcccacc aacagcatga ttgaccggaa 720
98 gccacgcctg ctcttcccca caaactccag cagtcaacct gtggccttgc agggccagtc 780
100 attaatcctg gagtgcattg ctgagggtt cctacacccc accatcaagt ggctgcaccc 840
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104 cctcaatgtg ggcgaggaag atgatggcga gtatacctgc cttgctgaga actcactggg 960
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126 gatcacacaa ggaccccgga gcacaattga gaagaaaggt gcaaggggtga cattcacgtg 1620
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150 acaagagacc tggaaggaac agaccgtgag cgaccccttc ctggtggtgt ctaacacttc 2340
152 cacatttgtg ccttatgaga tcaaagtcca ggcagtgaac aaccagggga agggccctga 2400
154 gcccagggtc accattggct attcagggga agactacccc caggtagacc ctgagcttga 2460
156 agacatcaca atcttcaact caagcactgt gctggtcagg tggaggcctg tggacttggc 2520
158 ccaggttaag ggccacctca ggggatacaa tgtaacgtac tgggtggaagg gcagtcagag 2580
160 aaagcacagc aagaggcatg tccacaaaag tcacatggtg gtacctgcga acaccaccag 2640

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162 tgccatcctc agtgggtttgc gtccttacag ctcttatcat gtggagggtac aggccttttaa 2700
164 tgggcggggc ttagggcctg caagtgaatg gaccttcagc accccagagg gagtgcctgg 2760
166 ccaccctgag gcattacatc tggagtgccg gtcggacact agcctgctac tgcactggca 2820
168 gccaccactc agccacaatg gagtgtcac tggctacctg ctctcttacc atcccttgga 2880
170 tggggaaagc aaagagcagt tgttcttcaa cctttcggac ccagagctcc ggactcataa 2940
172 tctcaccaac ctcaaccctg atctacagta ccgcttccag cttcaggcca ccaccaaca 3000
174 gggctcctgg gaggccattg tgcgtgaagg aggcactatg gccctatttg gcaagccaga 3060
176 ttttggcaac atttcagtca cagcagggtga aaactacagt gtgggtctcct ggggtccctcg 3120
178 ggaggggccag tgcaatttca gggtccacat cctgttcaaa gccttgccag aagggaaagt 3180
180 gagccctgat caccagcctc agcctcaata tgtgagctac aatcagagct cctacacaca 3240
182 gtgggacctc cagcctgaca ccaaatatga gatccacctg atgagggaga aggtcctctt 3300
184 gcaccatctg gctgtgaaga ctaatggcac tggccccgtg cgagtgtcga ctaccggtag 3360
186 ctttgccctc gagggtcgtg tcatcgctt tgctcagtgt atcattctct tgctcctcat 3420
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190 ggaggacctc caggtagatt ccgagggccg gcccatgaaa gacgagacct tcggcgagta 3540
192 caggtccctg gagagtgaca atgaagagaa ggccttcggc agcagccagc catctctcaa 3600
194 tggagacatc aaacccctag gcagtgatga cagtctggct gattatgggg gcagtgtgga 3660
196 tgtccagttc aatgaggatg gctctttcat cggccaatac agtggcaaaa aagagaagga 3720
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200 agaatagcaa gctcgag 3797
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 1259
205 <212> TYPE: PRT
206 <213> ORGANISM: Rattus rattus
208 <400> SEQUENCE: 5
210 Met Val Val Met Leu Arg Tyr Val Trp Pro Leu Leu Leu Cys Ser Pro
211 1 5 10 15
214 Cys Leu Leu Ile Gln Ile Pro Asp Glu Tyr Lys Gly His His Val Leu
215 20 25 30
218 Glu Pro Pro Val Ile Thr Glu Gln Ser Pro Arg Arg Leu Val Val Phe
219 35 40 45
222 Pro Thr Asp Asp Ile Ser Leu Lys Cys Glu Ala Arg Gly Arg Pro Gln
223 50 55 60
226 Val Glu Phe Arg Trp Thr Lys Asp Gly Ile His Phe Lys Pro Lys Glu
227 65 70 75 80
230 Glu Leu Gly Val Val Val His Glu Ala Pro Tyr Ser Gly Ser Phe Thr
231 85 90 95
234 Ile Glu Gly Asn Asn Ser Phe Ala Gln Arg Phe Gln Gly Ile Tyr Arg
235 100 105 110
238 Cys Tyr Ala Ser Asn Asn Leu Gly Thr Ala Met Ser His Glu Ile Gln
239 115 120 125
242 Leu Val Ala Glu Gly Ala Pro Lys Trp Pro Lys Glu Thr Val Lys Pro
243 130 135 140
246 Val Glu Val Glu Glu Gly Glu Ser Val Val Leu Pro Cys Asn Pro Pro
247 145 150 155 160
250 Pro Ser Ala Ala Pro Leu Arg Ile Tyr Trp Met Asn Ser Lys Ile Leu
251 165 170 175
254 His Ile Lys Gln Asp Glu Arg Val Ser Met Gly Gln Asn Gly Asp Leu
255 180 185 190

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258 Tyr Phe Ala Asn Val Leu Thr Ser Asp Asn His Ser Asp Tyr Ile Cys
259      195      200      205
262 Asn Ala His Phe Pro Gly Thr Arg Thr Ile Ile Gln Lys Glu Pro Ile
263      210      215      220
266 Asp Leu Arg Val Lys Pro Thr Asn Ser Met Ile Asp Arg Lys Pro Arg
267 225      230      235      240
270 Leu Leu Phe Pro Thr Asn Ser Ser Ser His Leu Val Ala Leu Gln Gly
271      245      250      255
274 Gln Ser Leu Ile Leu Glu Cys Ile Ala Glu Gly Phe Pro Thr Pro Thr
275      260      265      270
278 Ile Lys Trp Leu His Pro Ser Asp Pro Met Pro Thr Asp Arg Val Ile
279      275      280      285
282 Tyr Gln Asn His Asn Lys Thr Leu Gln Leu Leu Asn Val Gly Glu Glu
283      290      295      300
286 Asp Asp Gly Glu Tyr Thr Cys Leu Ala Glu Asn Ser Leu Gly Ser Ala
287 305      310      315      320
290 Arg His Ala Tyr Tyr Val Thr Val Glu Ala Ala Pro Tyr Trp Leu Gln
291      325      330      335
294 Lys Pro Gln Ser His Leu Tyr Gly Pro Gly Glu Thr Ala Arg Leu Asp
295      340      345      350
298 Cys Gln Val Gln Gly Arg Pro Gln Pro Glu Val Thr Trp Arg Ile Asn
299      355      360      365
302 Gly Met Ser Ile Glu Lys Val Asn Lys Asp Gln Lys Tyr Arg Ile Glu
303      370      375      380
306 Gln Gly Ser Leu Ile Leu Ser Asn Val Gln Pro Ser Asp Thr Met Val
307 385      390      395      400
310 Thr Gln Cys Glu Ala Arg Asn Gln His Gly Leu Leu Leu Ala Asn Ala
311      405      410      415
314 Tyr Ile Tyr Val Val Gln Leu Pro Ala Arg Ile Leu Thr Lys Asp Asn
315      420      425      430
318 Gln Thr Tyr Met Ala Val Glu Gly Ser Thr Ala Tyr Leu Leu Cys Lys
319      435      440      445
322 Ala Phe Gly Ala Pro Val Pro Ser Val Gln Trp Leu Asp Glu Glu Gly
323      450      455      460
326 Thr Thr Val Leu Gln Asp Glu Arg Phe Phe Pro Tyr Ala Asn Gly Thr
327 465      470      475      480
330 Leu Gly Ile Arg Asp Leu Gln Ala Asn Asp Thr Gly Arg Tyr Phe Cys
331      485      490      495
334 Gln Ala Ala Asn Asp Gln Asn Asn Val Thr Ile Leu Ala Asn Leu Gln
335      500      505      510
338 Val Lys Glu Ala Thr Gln Ile Thr Gln Gly Pro Arg Ser Thr Ile Glu
339      515      520      525
342 Lys Lys Gly Ala Arg Val Thr Phe Thr Cys Gln Ala Ser Phe Asp Pro
343      530      535      540
346 Ser Leu Gln Ala Ser Ile Thr Trp Arg Gly Asp Gly Arg Asp Leu Gln
347 545      550      555      560
350 Glu Arg Gly Asp Ser Asp Lys Tyr Phe Ile Glu Asp Gly Gln Leu Val
351      565      570      575
354 Ile Gln Ser Leu Asp Tyr Ser Asp Gln Gly Asn Tyr Ser Cys Val Ala

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355          580          585          590
358 Ser Thr Glu Leu Asp Glu Val Glu Ser Arg Ala Gln Leu Leu Val Val
359          595          600          605
362 Gly Ser Pro Gly Pro Val Pro His Leu Glu Leu Ser Asp Arg His Leu
363          610          615          620
366 Leu Lys Gln Ser Gln Val His Leu Ser Trp Ser Pro Ala Glu Asp His
367 625          630          635          640
370 Asn Ser Pro Ile Glu Lys Tyr Asp Ile Glu Phe Glu Asp Lys Glu Met
371          645          650          655
374 Ala Pro Glu Lys Trp Phe Ser Leu Gly Lys Val Pro Gly Asn Gln Thr
375          660          665          670
378 Ser Thr Thr Leu Lys Leu Ser Pro Tyr Val His Tyr Thr Phe Arg Val
379          675          680          685
382 Thr Ala Ile Asn Lys Tyr Gly Pro Gly Glu Pro Ser Pro Val Ser Glu
383          690          695          700
386 Thr Val Val Thr Pro Glu Ala Ala Pro Glu Lys Asn Pro Val Asp Val
387 705          710          715          720
390 Arg Gly Glu Gly Asn Glu Thr Asn Asn Met Val Ile Thr Trp Lys Pro
391          725          730          735
394 Leu Arg Trp Met Asp Trp Asn Ala Pro Gln Ile Gln Tyr Arg Val Gln
395          740          745          750
398 Trp Arg Pro Leu Gly Lys Gln Glu Thr Trp Lys Glu Gln Thr Val Ser
399          755          760          765
402 Asp Pro Phe Leu Val Val Ser Asn Thr Ser Thr Phe Val Pro Tyr Glu
403          770          775          780
406 Ile Lys Val Gln Ala Val Asn Asn Gln Gly Lys Gly Pro Glu Pro Gln
407 785          790          795          800
410 Val Thr Ile Gly Tyr Ser Gly Glu Asp Tyr Pro Gln Val Ser Pro Glu
411          805          810          815
414 Leu Glu Asp Ile Thr Ile Phe Asn Ser Ser Thr Val Leu Val Arg Trp
415          820          825          830
418 Arg Pro Val Asp Leu Ala Gln Val Lys Gly His Leu Arg Gly Tyr Asn
419          835          840          845
422 Val Thr Tyr Trp Trp Lys Gly Ser Gln Arg Lys His Ser Lys Arg His
423          850          855          860
426 Val His Lys Ser His Met Val Val Pro Ala Asn Thr Thr Ser Ala Ile
427 865          870          875          880
430 Leu Ser Gly Leu Arg Pro Tyr Ser Ser Tyr His Val Glu Val Gln Ala
431          885          890          895
434 Phe Asn Gly Arg Gly Leu Gly Pro Ala Ser Glu Trp Thr Phe Ser Thr
435          900          905          910
438 Pro Glu Gly Val Pro Gly His Pro Glu Ala Leu His Leu Glu Cys Gln
439          915          920          925
442 Ser Asp Thr Ser Leu Leu Leu His Trp Gln Pro Pro Leu Ser His Asn
443          930          935          940
446 Gly Val Leu Thr Gly Tyr Leu Leu Ser Tyr His Pro Leu Asp Gly Glu
447 945          950          955          960
450 Ser Lys Glu Gln Leu Phe Phe Asn Leu Ser Asp Pro Glu Leu Arg Thr
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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date